IAP17 RADEMARK OFFICE
OIPE IAP17 OCT 24 2006 PATENT & TRADEMARK OFFICE

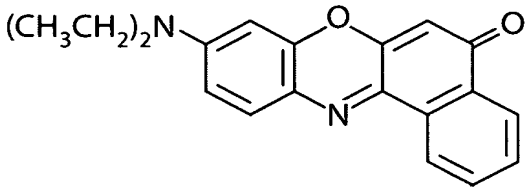


Fig. 1A

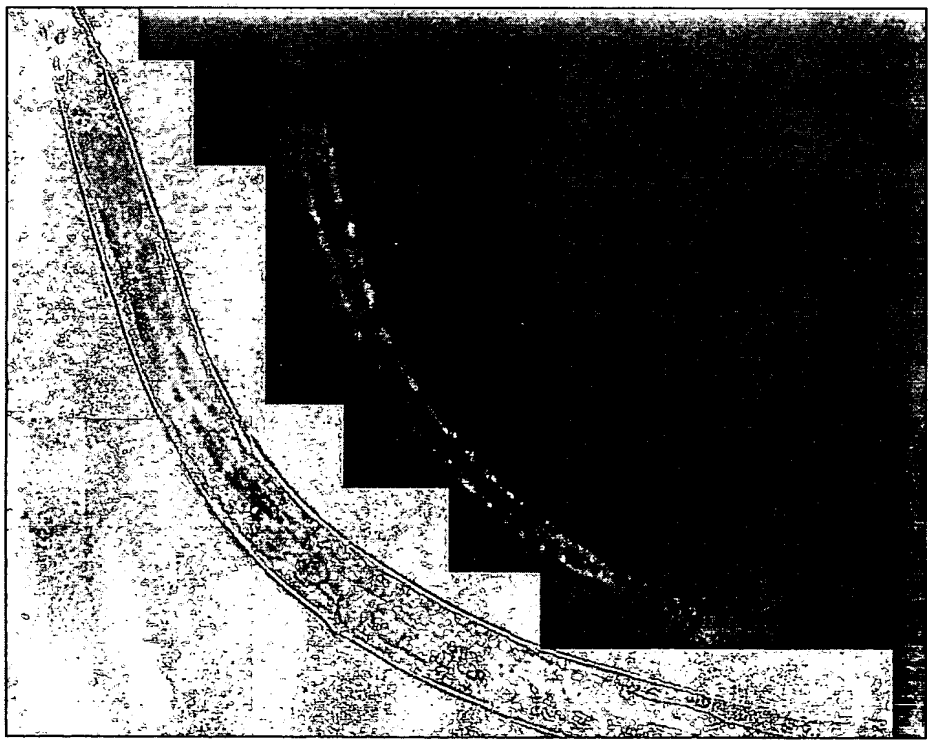


Fig. 1B

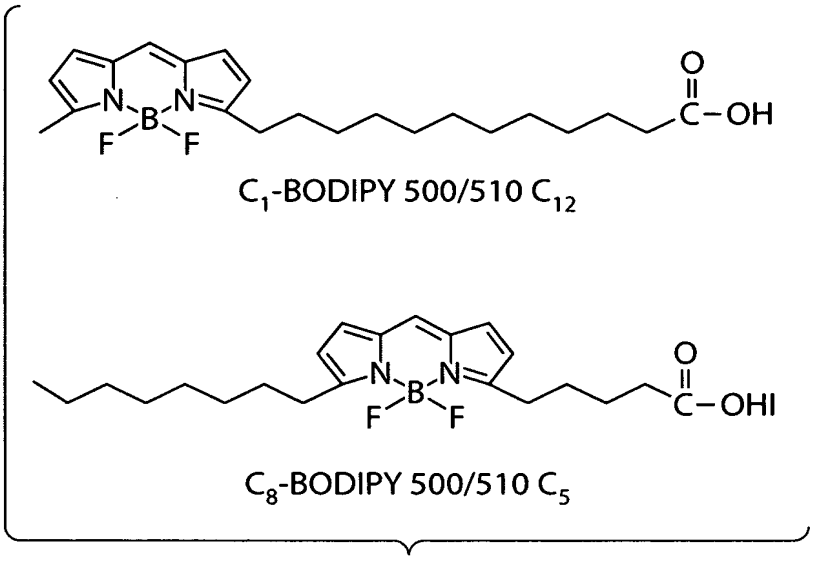


Fig. 2A

Fig. 2B

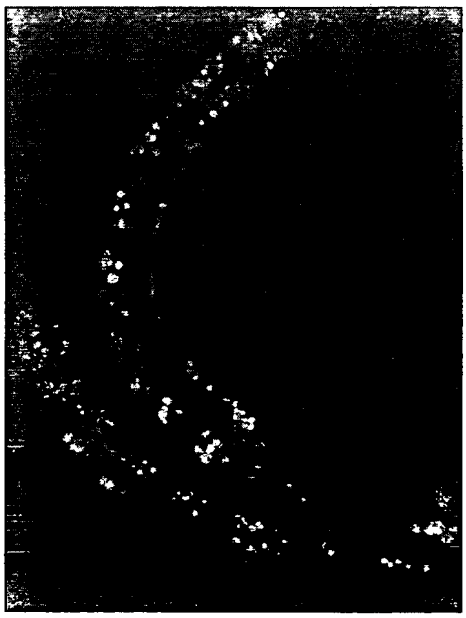


Fig. 2C

Fig. 2D

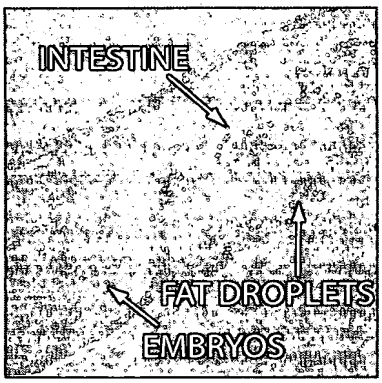


Fig. 3A

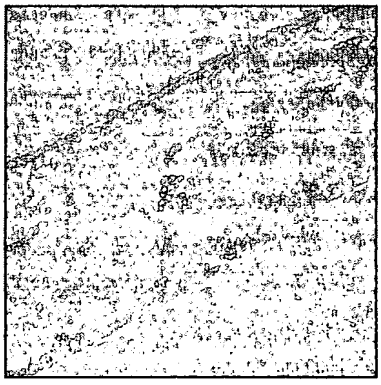
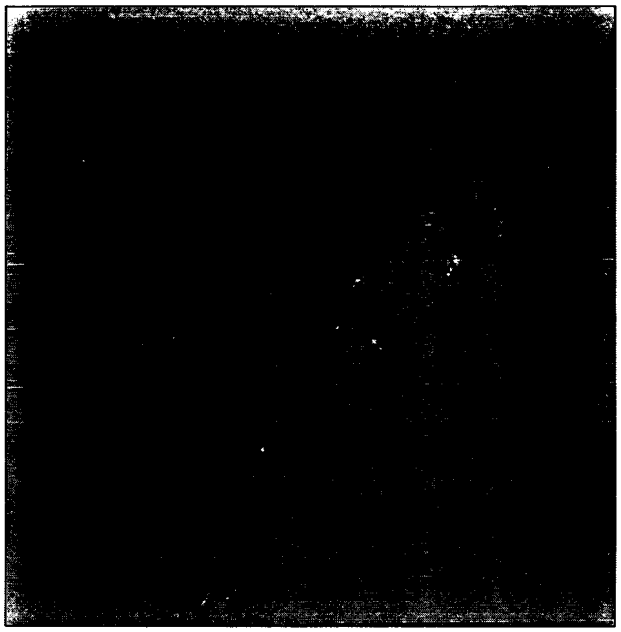


Fig. 3B



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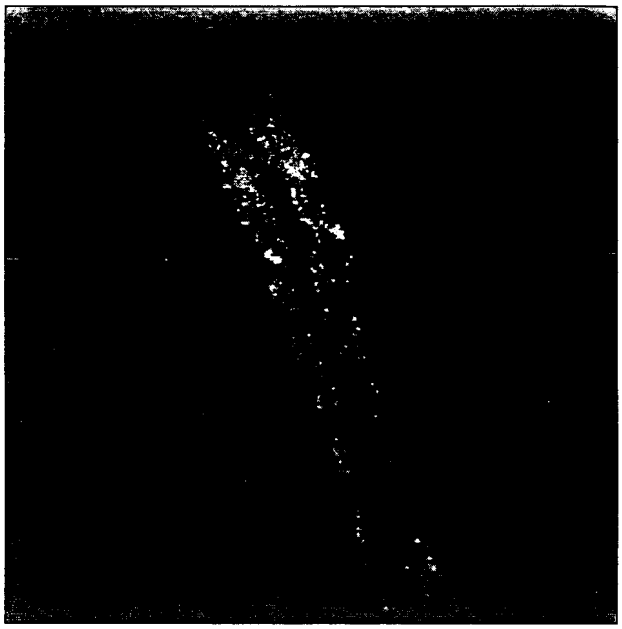


Fig. 4B

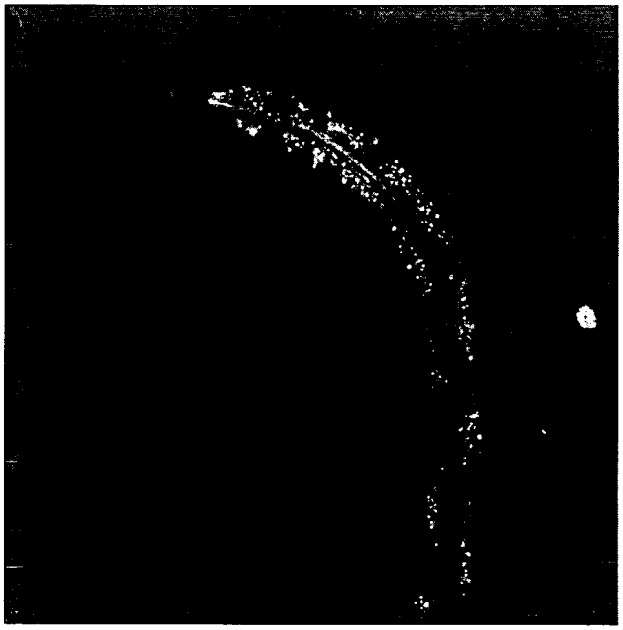


Fig. 4C

Fig. 5A

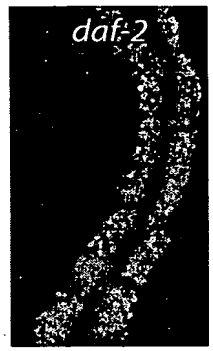


Fig. 5B

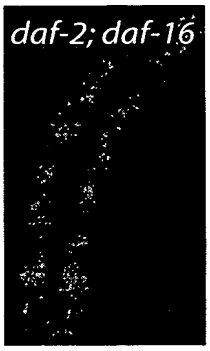


Fig. 5C

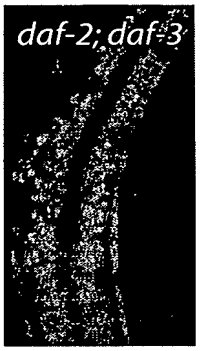


Fig. 5D

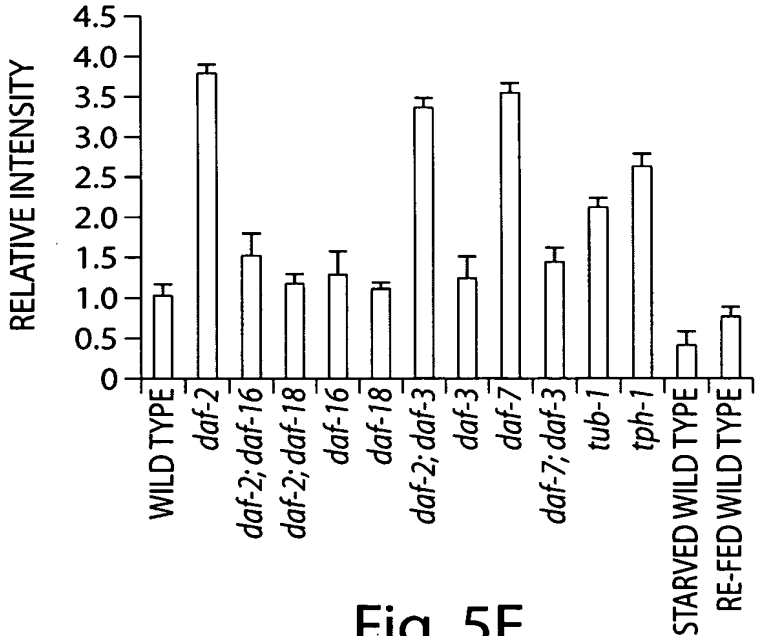


Fig. 5E

Fig. 6A

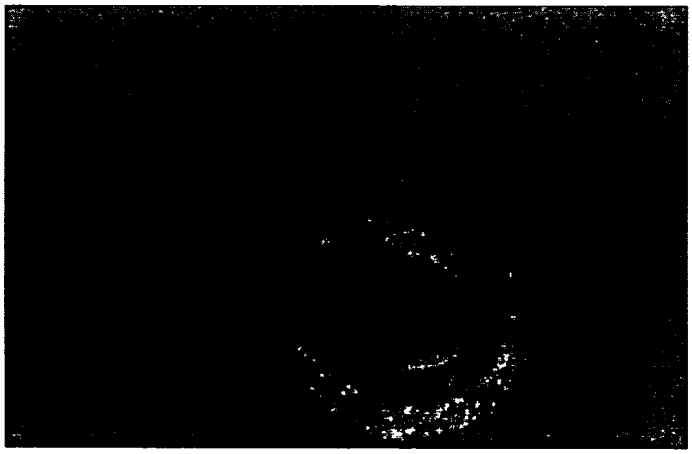


Fig. 6B

Fig. 6C

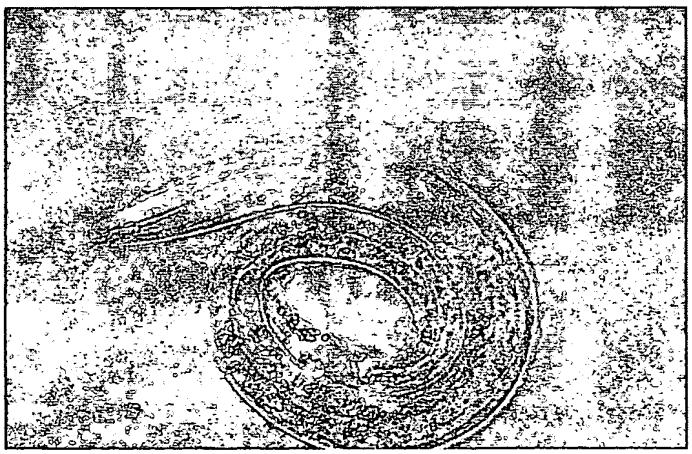
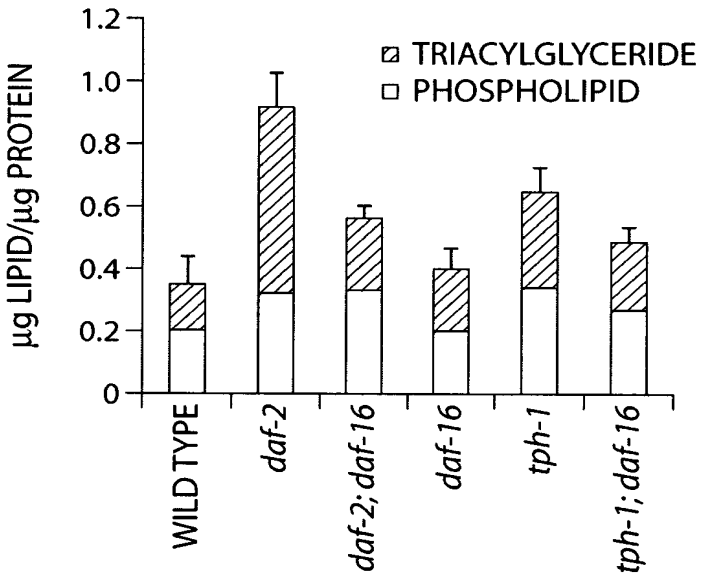


Fig. 6D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0.6
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0.2
0
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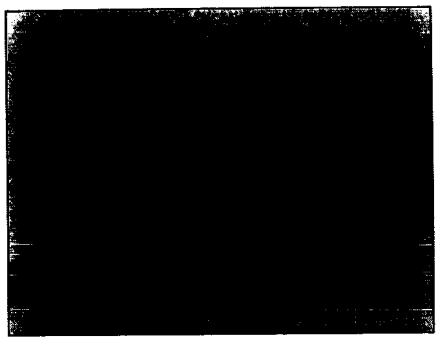
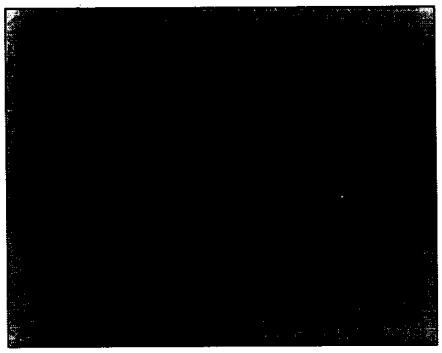
TRIACYLGLYCERIDE
PHOSPHOLIPID
WILD TYPE
daf-2
daf-2;daf-16
daf-16
tph-1
tph-1;daf-16

Fig. 7



WILD TYPE

Fig. 8A



WILD TYPE

AICAR

Fig. 8B

WILD TYPE

STARVED

Fig. 8C

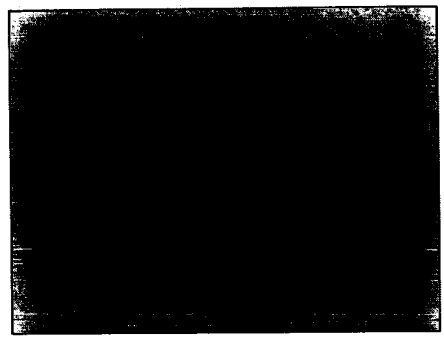
daf-2(e1370)

Fig. 8D

daf-2(e1370)

AICAR

Fig. 8E



daf-2(e1370)

STARVED

Fig. 8F

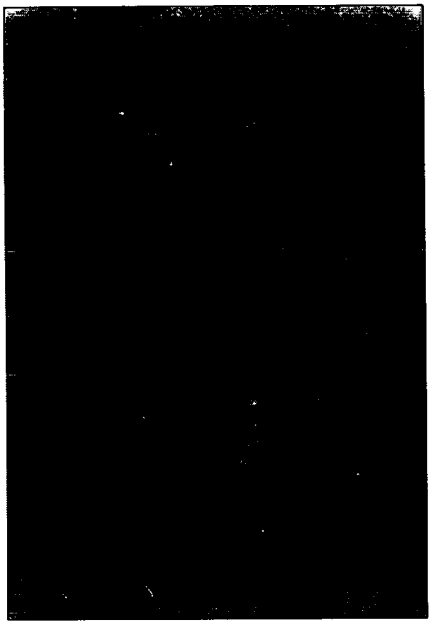


Fig. 9A

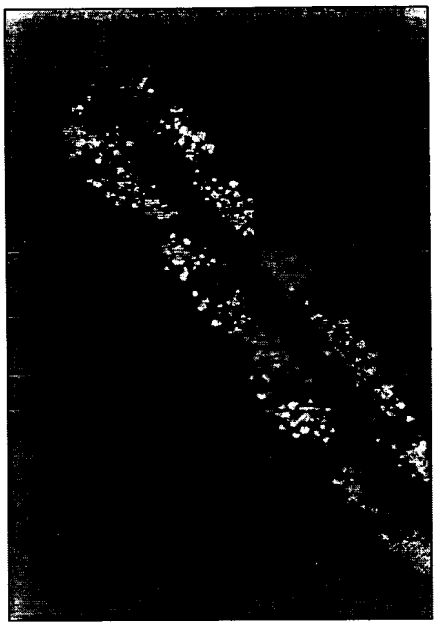


Fig. 9B

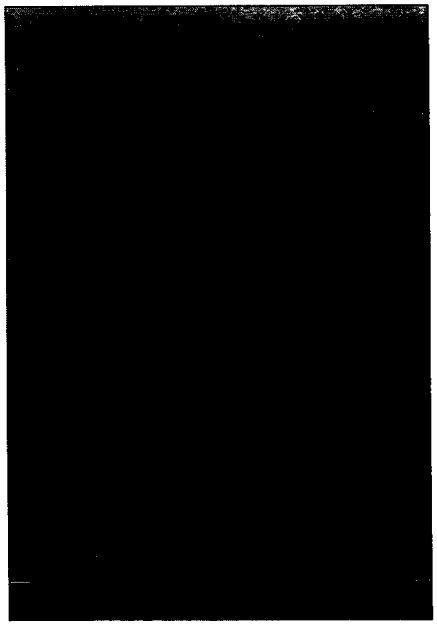


Fig. 9C

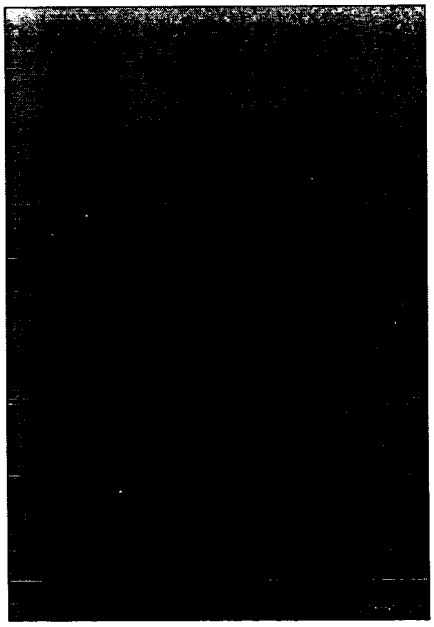


Fig. 9D

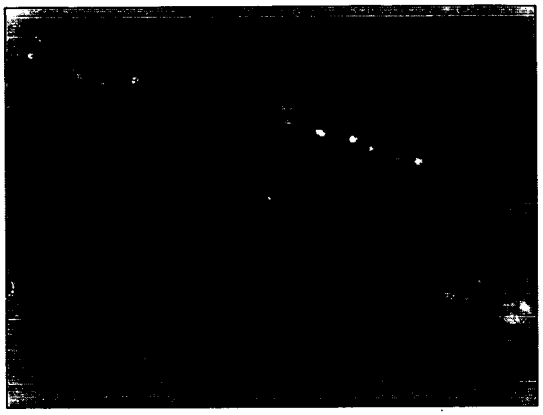


Fig. 9E

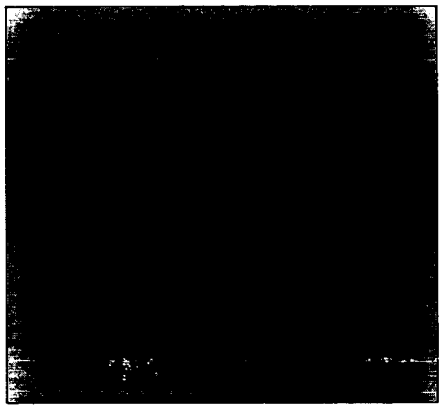
Fig. 9F

Fig. 9G

C12-BODIPY

lpo-2

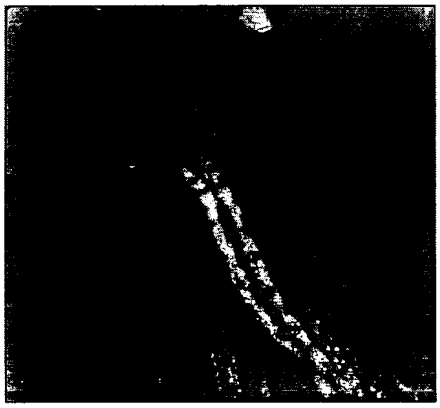
Fig. 10E



NILE RED

lpo-2

Fig. 10F



C12-BODIPY

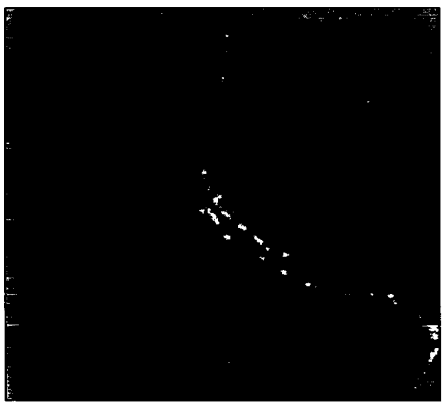
lpo-1

Fig. 10C

NILE RED

lpo-1

Fig. 10D



C12-BODIPY

WILD TYPE

Fig. 10A

NILE RED

WILD TYPE

Fig. 10B

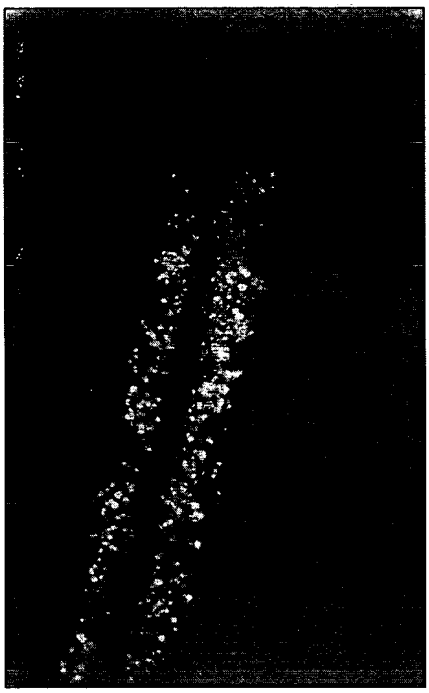


Fig. 11A

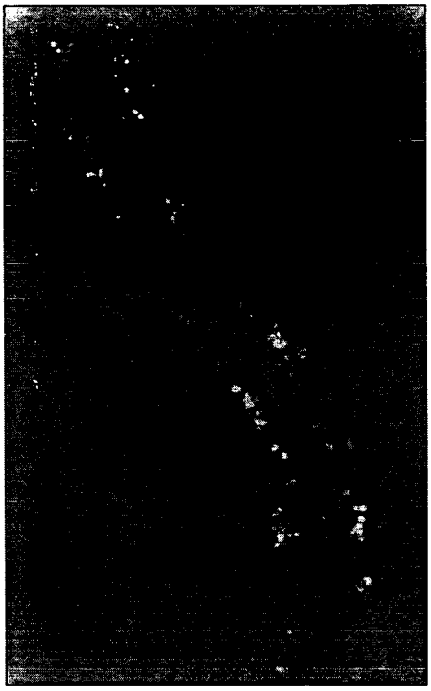


Fig. 11B

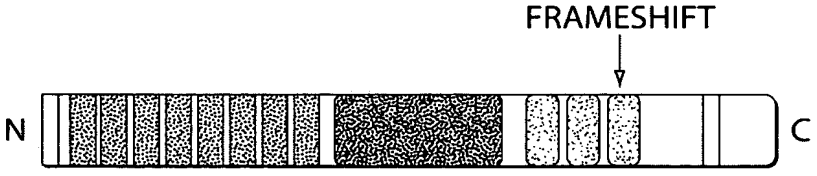


Fig. 11C

lpo-1 genomic
SEQ ID NO:1

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Fig. 11D

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Fig. 11D Cont.

lpo-1 cDNA
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ga

Fig. 11E

LPO-1
SEQ ID NO:3

MRTCLTLTGF LLISMATISV GLQPMGAPTR KCDATNSFQC QDGRCIPMSW RCDGDIDCQN EEDEKNCPKV
CGAEEHKCGE VKSARSSLER FKCIPNKWVC DGEFDCEDKS DEFQCKNVSC QEKQFQCEEL SGDYSLCIPE
TWVCDGQRDC TNGKDEQNCT SKTSKCPDNN FQCSNGNCIF KNWVCDGEED CSDGSDELLT APSNCNRTVN
QCPPGEMWKC GSGECIPSRW RCDAEVDCKD HSDEKNCTAI QHTCKLAEEF ACKASHNCIN KAFVCDGELD
CSDGSDEDDC ADVRTECKSG ERTCPASYGA YGAESGHVVC IPASSWCNGE EDCPDGGDEK ECNMTAPVTC
QKGTEYECPS TPLQCIEMSK LCASAQFDCG DGNMSVCSQK KIIEMCKPSS EGCVCRPSFV RGNNVCHCKD
GYKLENGQCI DINECEIAGV CDQICLNIPG SYRCACHAGY QISFGDTKIG SGRIANKCRA MGGDPLVLLT
NRHTIRQFDL VNKMHFPVSS SPGSAVAMDF HILNGTLIWS DVLSKQILKC SIGNVSNAFL GTDMCDKKHE
IVLTGDKIHT PDGLAVDWVH DLLFWTDGGL DQINVLDMKN GKQRVLYSSD LEEPRAIAVD PEVGLIFWTD
WGKKARIERS GMDGQHRTVI VEGDRVVWPN GLALDYVDKR VYWLMPRSSQ SSVFTGADIR TVMDQVKSPM
TVRIYHKQAQ PLMQNKCENS ECDHLCLPRA VYREKERVHE KTWHDRPFSC ACEGTTASDV LECFADLETK
SGISMFTIFL LLCVGGVVAA GFVIVRRKMG PRTFTALNFD NPIYRRTTEE ADHQMEDPFR DPFAEPRNGR
GRNDGLPTLA SADNETRADA LSF

Fig. 11F

```
     RAT      MGTSARWALWLLLALCWAPRDSGATASGKKAKCDSSQFQCTNGRCITLLWKCDGDEDCTD 60   (SEQ ID NO:10)
     human    MGTSALWALWLLLALCWAPRESGATGTGRKAKCEPSQFQCTNGRCITLLWKCDGDEDCVD 60   (SEQ ID NO:9)
5    lpo-1    MRTCLTLTGFLLISMATISVGLQPMGAPTRKCDATNSFQCQDGRCIPMSWRCDGDIDCQN 60   (SEQ ID NO:3)
              * *.   : :**:::.  .    . .:  :    ...*** :****.: *:**** ** :

     RAT      GSDEKNCVKKTCAESDFVCKNG---------QCVPNRWQCDGDPDCEDGSDESPEQCHMR 111
     human    GSDEKNCVKKTCAESDFVCNNG---------QCVPSRWKCDGDPDCEDGSDESPEQCHMR 111
10   lpo-1    EEDEKNCPKVCGAEEHKCGEVKSARSSLERFKCIPNKWVCDGEFDCEDKSDE--FQCKNV 118
                .***** *   **..   :  :: :: .  :*:*.:* ***: **** ***   **:

     RAT      TCRINEISCGARS---TQCIPESWRCDGENDCDNGEDEENCGNIT--CSADEFTCSSGRC 166
     human    TCRIHEISCGAHS---TQCIPVSWRCDGENDCDSGEDEENCGNIT--CSPDEFTCSSGRC 166
15   lpo-1    SCQEKQFQCEELSGDYSLCIPETWVCDGQRDCTNGKDEQNCTSKTSKCPDNNFQCSNGNC 178
              :*: :::.*   *.. : *** :* ***:.** .*:**:** . *:.*. ::* **.*.*

     RAT      VSRNFVCNGQDDCDDGSDELDCAPPTCG--------AHEFQCRTSSCIPLSWVCDDDADC 218
     human    ISRNFVCNGQDDCSDGSDELDCAPPTCG--------AHEFQCSTSSCIPISWVCDDDADC 218
20   lpo-1    IFKNWVCDGEEDCSDGSDELLTAPSNCNRTVNQCPPGEMWKCGSGECIPSRWRCDAEVDC 238
              : :*:**:*::**.******  **..*. : ..... ::* :..***  * ** :.**

     RAT      SDQSDESLEQCGRQPVIHTKCPTSEIQCGSGE-CIHKKWRCDGDPDCKDGSDEVNCPSR- 276
     human    SDQSDESLEQCGRQPVIHTKCPASEIQCGSGE-CIHKKWRCDGDPDCKDGSDEVNCPSR- 276
25   lpo-1    KDHSDE----KNCTAIQHTCKLAEEFACKASHNCINKAFVCDGELDCSDGSDEDDCADVR 294
              .*:***     .  .: **   :.*: * :...**:* : ***: **.***** :*..

     RAT      -TCRPDQFECEDGS----------CIHGSRQCNGIRDCVDGSDEVNCKNVN--QCLGPG 322
     human    -TCRPDQFECEDGS----------CIHGSRQCNGIRDCVDGSDEVNCKNVN--QCLGPG 322
30   lpo-1    TECKSGERTCPASYGAYGAESGHVVCIPASSWCNGEEDCPDGGDEKECNMTAPVTCQKGT 354
              : *:..:  *  . .: .:.:.   ** .*  *** .** **.** :*: . .  *

     RAT      KFKCRSG--ECIDITKVCD-QEQDCRDWSDEPLKECHINECLVNNGGCSHICKDLVIG-Y 378
     human    KFKCRSG--ECIDISKVCN-QEQDCRDWSDEPLKECHINECLVNNGGCSHICKDLVIG-Y 378
35   lpo-1    EYECPSTPLQCIEMSKLCASAQFDCGDGNMSVCSQKKIIEMCKPSSEGCVCRPSFVRGNN 414
              :::* * . :**:::*:* : : ** * . .  .: :* *    ..  .    .:* *.

     RAT      ECDCAAGFELIDRKTCGDIDECQNPGICSQICINLKGGYKCECSRGYQMDLATG------ 432
     human    ECDCAAGFELIDRKTCGDIDECQNPGICSQICINLKGGYKCECSRGYQMDLATG------ 432
40   lpo-1    VCHCKDGYKLEN-GQCIDINECEIAGVCDQICLNIPGSYRCACHAGYQISFGDTKIGSGR 473
               *.*  *::* :   * **:**: .*:*.***:*: *.*:* *  ***:.:.  . .:.

     RAT      ---VCKAVGKEPSLIFTNRRDIRKIGLERKEYIQLVEQLRNTVALDADIAAQKLFWADLS 489
     human    ---VCKAVGKEPSLIFTNRRDIRKIGLERKEYIQLVEQLRNTVALDADIAAQKLFWADLS 489
45   lpo-1    IANKCRAMGGDPLVLLTNRHTIRQFDLVNKMHFPVSSSPGSAVAMDFHILNGTLIWSDVL 533
               :. *:*:* :* :::***: **::.* .* :: : ..  .:**:* .*   .*:*:*:

     RAT      QKAIFSASID-----------DKVGRHFKMIDNVYNPAAIAVDWVYKTIYWTDAASKTI 537
     human    QKAIFSASID-----------DKVGRHVKMIDNVYNPAAIAVDWVYKTIYWTDAASKTI 537
50   lpo-1    SKQILKCSIGNVSNAFLGTDMCDKKHEIVLTGDKIHTPDGLAVDWVHDLLFWTDGGLDQI 593
              .* *:..**.. :.:  .:. .**  . .   *:::.* .:*****:. ::***.. . *
```

Fig. 11G

```
     RAT          SVATLDGTKRKFLFNSDLREPASIAVDPLSGFVYWSDWGEPAKIEKAGMNGFDRRPLVTE 597
     human        SVATLDGTKRKFLFNSDLREPASIAVDPLSGFVYWSDWGEPAKIEKAGMNGFDRRPLVTA 597
 5   lpo-1        NVLDMKNGKQRVLYSSDLEEPRAIAVDPEVGLIFWTDWGKKARIERSGMDGQHRTVIVEG 653
                  .*  :.. *::.*:.***.** :***** *:::*:***: *:**::**:* .*  :*

     RAT          D-IQWPNGITLDLVKSRLYWLDSKLHMLSSVDLNGQDRRIVLKSLEFLAHPLALTIFEDR 656
     human        D-IQWPNGITLDLIKSRLYWLDSKLHMLSSVDLNGQDRRIVLKSLEFLAHPLALTIFEDR 656
10   lpo-1        DRVVWPNGLALDYVDKRVYWLMPRSSQSS------------------------------ 682
                  * : ****::** :..*:*** .:    *

     RAT          VYWIDGENEAVYGANKFTGSELATLVNNLNDAQDIIIYHELVQPSGKNWCEEDMENGGCE 716
     human        VYWIDGENEAVYGANKFTGSELATLVNNLNDAQDIIVYHELVQPSGKNWCEEDMENGGCE 716
15   lpo-1        --------------VFTGADIRTVMDQVKSPMTVRIYHKQAQPLMQNKCENSE----CD 723
                               ***::: *:::::::.  : :**: .**  :* **:.     *:

     RAT          YLCLPAPQINDHSPKYTCSCPNGYNLEENGRECQSTSTPVTYSETKDVNTTDILRTSGLV 776
     human        YLCLPAPQINDHSPKYTCSCPSGYNVEENGRDCQSTATTVTYSETKDTNTTEISATSGLV 776
20   lpo-1        HLCLPRAVYREKE------------RVHEKTWHDRPFSCACEGTTASDVLECFADLETK 770
                  :**** .  .::.             . : :  :. . . : . *.  :. :

     RAT          PGGINVTTAVSEVSVPPKGTSAAWAILPLLLLVMAAVGGYLMWRNWQHKNMKSMNFDNPV 836
     human        PGGINVTTAVSEVSVPPKGTSAAWAILPLLLLVMAAVGGYLMWRNWQHKNMKSMNFDNPV 836
25   lpo-1        SG----------------ISMFTIFLLLCVGGVVAAGFVIVRRKMGPRTFTALNFDNPI 813
                  .*                 *    :* * :  :.*.*  :: *:   :.:.::*****:

     RAT          YLKTTEEDLSIDIG---------RHSASVGHTYPAISVVSTDDDLA---- 873
     human        YLKTTEEDLSIDIG---------RHSASVGHTYPAISVVSTDDDLA---- 873
30   lpo-1        YRRTTEEADHQMEDPFRDPFAEPRNGRGRNDGLPTLASADNETRADALSF 863
                  * :
```

Fig. 11G Cont.

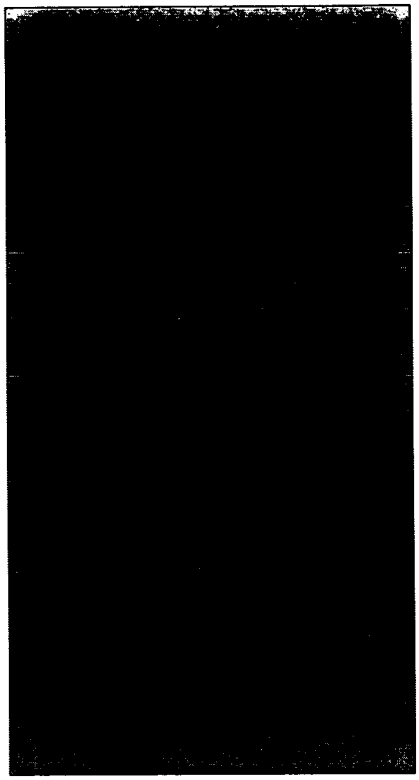

Fig. 12A

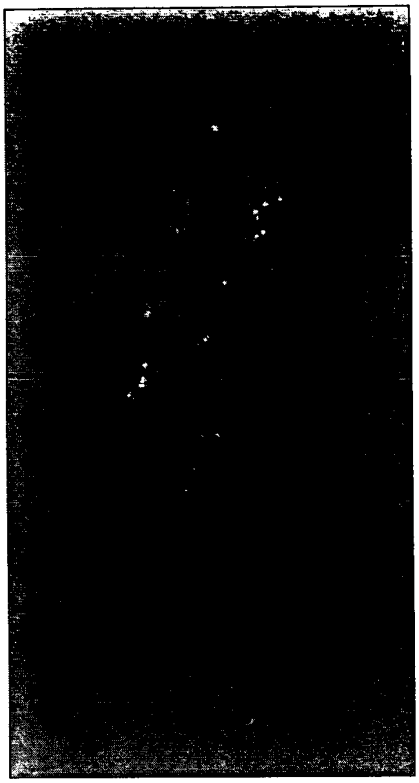

Fig. 12B

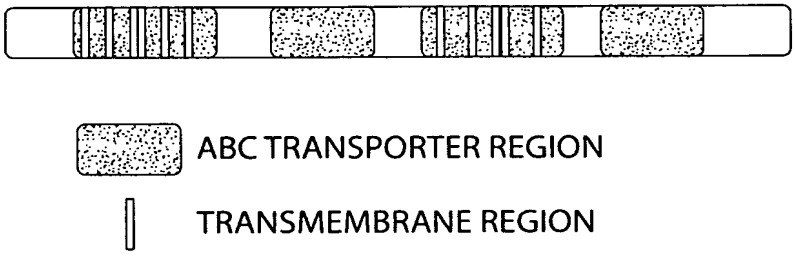

Fig. 12C

LPO-3 Unspliced DNA (7496 bp)
SEQ ID NO:4

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gaaaagaaac atcaacagaa aacaatgaat tgatcactac aattatataa atttgctttt cttcctatca
catatcactt cgtctgtctg cgtctctatc actttattat cttcaatatc ccacattatc tcggttggcc
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aaaattggaa gaaaaaagag aaataaaaaa ggggtggagc ctagacacct tcaacacata tttttaatta
aagacgccct tttttcggaa gacctttctc tccgctttcc ccccattatt ttctattatt atctaactg
ATGAAAAGCC GAAAAAACGA GCCCACTTGG GTGACTAAGC CTCTGCTTAA ACGgtatgag ttgtcaagag
attctctgaa aaaaacctaa aatttttgaa tattcaaaac agataatttc agattctagt aatttgtgat
aattccaaaa taaaaaatat aaacatttta cagCTCTCAT TCAAGTGACT CTTCAATCGA TGAATCAACT
GTTAAACTCA CAAATTATGG GATATTCTAT TACACTCAAG GAGTTGATCT ACTTCTTTTA ATTACTGGAA
CAGTTGCAGC AGTTATTCAT GGAGCTGGTT TTCCGTTACT TGCTATTGgt atgtggtttt atttttaat
ttgaatgata aatcaaaagc tgaaattatc atttgaaacg tcaactacat ataattttat aaaatgttat
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catatatttc atattccagC CATTGCACGT GCTCTTGTCA AAAATCCAAA AATCCTTTTG CTCGACGAAG
```

Fig. 12D

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AAATGTTACA TATCAAGAAA TTGTTGAAGC TGCCAAAATG GCAAATATTC ACAATTTCAT TCTAGGATTG
CCAGATgtag ggtgatattt tcataaatca gaactcattc taaaaatttc agGGTTATGA TACTCATGTC
GGAGAGAAAG GAACTCAACT TTCGGGTGGT CAAAAACAAA GAATTGCCAT TGCACGGGCA CTTGTTCGAT
CTCCTTCTGT TTTACTTTTG GATGAAGCAA CTAGTGCATT AGATACGGAA AGTGAAAAGg tttgtatgaa
aaatattgaa atagcaaatt gactttgaag aatatcgttt tattcactgt ttacagATTG TACAAGAAGC
ATTGGACGCC GCAAAACAAG GTCGCACGTG TCTTGTCATT GCTCATCGGT TGAGCACAAT TCAAAATAGT
GACGTCATTG CGATCGTCAG TGAGGGTAAA ATTGTGGAAA AGGGAACACA TGACGAGTTG ATAAGGAAGA
GTGAAATATA TCAGAAATTC TGTGAAACGC AGAGGATTGT CGAAAGTCAA TAAtttaaat atgtattaga
ttctcaaaca cgagtttaca aactaatttg catggagttt cattttttta atgttcaatt gaaacagctt
gatatttaaa atttaaatat gctcatcaag taaaattttt agaaaatttt gtaaacccgt aataattttt
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taccat

Fig. 12D Cont.

lpo-3
SEQ ID NO:5

```
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ctcggaggaa tgacaacagt gtttttacga gctcaaaact cggatttcgt cgttggtgtg gataatgtga
acccggaagg attggtcccg atatctctag atgaattcaa ctcggaagtt gtcaagtatt gtatctacta
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gcatggcaac gcgaacaaga gttgaacaag aaacgtatgc agtcgctggt gcaattgcag aagaaacatt
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accaattgat gtctatcgag tattctttgc tatttcattc tgtggacaaa tgattggaaa tactacatct
tttattcctg atgtcgtaaa agctcgtctt gctgcttctc ttttgttcta tcttattgaa catccaacac
ctattgattc tctatctgat agtggaattg tgaagccgat aactggaaat atttcaatca gaaatgtatt
tttcaattat ccaacaagaa aggataccaa ggttttacaa ggattcactc ttgatatcaa agccggtaaa
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ggaaaaggga acacatgacg agttgataag gaagagtgaa atatatcaga aattctgtga aacgcagagg
attgtcgaaa gtcaataa
```

Fig. 12E

LPO-3
SEQ ID NO:6

MKSRKNEPTW VTKPLLKRSH SSDSSIDEST VKLTNYGIFY YTQGVDLLLL ITGTVAAVIH GAGFPLLAIV
LGGMTTVFLR AQNSDFVVGV DNVNPEGLVP ISLDEFNSEV VKYCIYYLVL GVLMFFTSYV QIACFESYAE
RLVHKLRQNY LKAILRQQIQ WFDKQQTGNL TARLTDDLER VERGLGDKFA LLVQMFAAFL AGYGVGFFYS
WSMTLVMMGF APLIVLSGAK MSKSMATRTR VEQETYAVAG AIAEETFSSI RTVHSLNGHK RELDRFYNAL
EVGRQTGIVK YCYMGIGVGF SNLCMYSSYA LAFWYGSTLI INDPTFDRGL IFTVFFAVLS GSTSLGGALP
HLASFGTARG AASTVLRVIN SHPKIDPYSL EGILVDNMKG DISFKDVHFR YPSRKDIHVL KGISLELKAG
DKIALVGSSG CGKSTIVNLL QRFYDPTKGR VLIDGVDLRE VNVHSLREQI GIVSQEPVLF DGTIYENIKM
GNEHATHDQV VEACKMANAN DFIKRLPDGY GTRVGEKGVQ LSGGQKQRIA IARALVKNPK ILLLDEATSA
LDTEAEREVQ GALDQAQAGR TTIIVAHRLS TIRNVDRIFV FKAGNIVESG SHEELMSKQG IFYDMTQAQV
VRQQQQEAGK DIEDTISESA HSHLSRKSST RSAISIATSI HQLAEEVEEC KAPPTSMFKI FKFNGDKVGW
FIGGIFGAFI FGSVTPVFAL VYAEIFNVYS LPADQMQANV YFWCGMFVLM GITFFVGFFT SANCLGRCGE
SLTMKLRFEA FKNLLRQDIA FYDDLRHGTG KLCTRFATDA PNVRYVFTRL PVVLASIVTI CGALGIGFYY
GWQLALILVV MVPLLVMGGY FEMQMRFGKQ IRDTQLLEEA GKVASQAVEH IRTVHSLNRQ EQFHFTYCEY
LREPFNTNLK HAHTYGAVFA FSQSLIFFMY AAAFYLGSIF VNQQAMQPID VYRVFFAISF CGQMIGNTTS
FIPDVVKARL AASLLFYLIE HPTPIDSLSD SGIVKPITGN ISIRNVFFNY PTRKDTKVLQ GFTLDIKAGK
TVALVGHSGC GKSTIMGLLE RFYNQDKGMI MIDGDNIRNL NISSLREQVC IVSQEPTLFD CTIGENICYG
TNRNVTYQEI VEAAKMANIH NFILGLPDGY DTHVGEKGTQ LSGGQKQRIA IARALVRSPS VLLLDEATSA
LDTESEKIVQ EALDAAKQGR TCLVIAHRLS TIQNSDVIAI VSEGKIVEKG THDELIRKSE IYQKFCETQR
IVESQ

Fig. 12F

```
     human   MDLEGDRNGGAKKKNFFKLNNKSEKDKKEKKPTVSVFSMFRYSNWLDKLYMVVGTLAAII 60   SEQ ID NO:11
     MOUSE   MEFEENLKGRADK-NFSKMGKKSKKEKKEKKPAVGVFGMFRYADWLDKLCMILGTLAAII 59   SEQ ID NO:12
5    LPO-3   MKSRKNEPTWVTK-PLLKRSHSSDSSIDESTVKLTNYGIFYYTQGVDLLLLITGTVAAVI 59   SEQ ID NO:6
             *. . :    . *. : * .:.*... .*..  :  :.:* *:: :* * :: **:**:*

     human   HGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFFMN--LEEDMTRYAYYY 118
     MOUSE   HGTLLPLLMLVFGNMTDSFTKA--EASILPSITNQSGPNSTLIISNSSLEEEMAIYAYYY 117
10   LPO-3   HGAGFPLLAIVLGGMTTVFLRAQ-NSDFVVGVDN-VNPEGLVPISLDEFNSEVVKYCIYY 117
             **: :**: :*:* **  * .* .  .:: .: *  . :.   :    ::.::. *. **

     human   SGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMRQEIGWFDVHDVGELNTRLTDD 178
     MOUSE   TGIGAGVLIVAYIQVSLWCLAAGRQIHKIRQKFFHAIMNQEIGWFDVHDVGELNTRLTDD 177
15   LPO-3   LVLGVLMFFTSYVQIACFESYAERLVHKLRQNYLKAILRQQIQWFDKQQTGNLTARLTDD 177
               :*. ::..:*:*:: :   * * :**:*:::::**:.*:* *** ::.*:*.:*****

     human   VSKINEGIGDKIGMFFQSMATFFTGFIVGFTRGWKLTLVILAISPVLGLSAAVWAKILSS 238
     MOUSE   VSKINDGIGDKIGMFFQSITTFLAGFIIGFISGWKLTLVILAVSPLIGLSSALWAKVLTS 237
20   LPO-3   LERVREGLGDKFALLVQMFAAFLAGYGVGFFYSWSMTLVMMGFAPLIVLSGAKMSKSMAT 237
             :.::.:*:***:.::.* :::*::*: :**  .*.:***::..:*:: **.*  :* :::

     human   FTDKELLAYAKAGAVAEEVLAAIRTVIAFGGQKKELERYNKNLEEAKRIGIKKAITANIS 298
     MOUSE   FTNKELQAYAKAGAVAEEVLAAIRTVIAFGGQQKELERYNKNLEEAKNVGIKKAITASIS 297
25   LPO-3   RTRVEQETYAVAGAIAEETFSSIRTVHSLNGHKRELDRFYNALEVGRQTGIVKYCYMGIG 297
              *  *  :** ***:***.:::**** ::.*:::**:*: : ** .:. ** *    .*.

     human   IGAAFLLIYASYALAFWYGTTLVLSG-EYSIGQVLTVFFSVLIGAFSVGQASPSIEAFAN 357
     MOUSE   IGIAYLLVYASYALAFWYGTSLVLSN-EYSIGEVLTVFFSILLGTFSIGHLAPNIEAFAN 356
30   LPO-3   VGFSNLCMYSSYALAFWYGSTLIINDPTFDRGLIFTVFFAVLSGSTSLGGALPHLASFGT 357
             :* : * :*:*********::*::..  :. * ::****::* *: *:*   * : :*..

     human   ARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 417
     MOUSE   ARGAAFEIFKIIDNEPSIDSFSTKGYKPDSIMGNLEFKNVHFNYPSRSEVQILKGLNLKV 416
35   LPO-3   ARGAASTVLRVINSHPKIDPYSLEGILVDNMKGDISFKDVHFRYPSRKDIHVLKGISLEL 417
             *****  ::::*:..*.**.:* .*   *.: *::.*::*** ****.::::***:.*::

     human   QSGQTVALVGNSGCGKSTTVQLMQRLYDPTEGMVSVDGQDIRTINVRFLREIIGVVSQEP 477
     MOUSE   KSGQTVALVGNSGCGKSTTVQLMQRLYDPLEGVVSIDGQDIRTINVRYLREIIGVVSQEP 476
40   LPO-3   KAGDKIALVGSSGCGKSTIVNLLQRFYDPTKGRVLIDGVDLREVNVHSLREQIGIVSQEP 477
             ::*:.:****.******* *:*:**:*** :* * :** *:* :**: *** **:*****

     human   VLFATTIAENIRYGRENVTMDEIEKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQ 537
     MOUSE   VLFATTIAENIRYGREDVTMDEIEKAVKEANAYDFIMKLPHQFDTLVGERGAQLSGGQKQ 536
45   LPO-3   VLFDGTIYENIKMGNEHATHDQVVEACKMANANDFIKRLPDGYGTRVGEKGVQLSGGQKQ 537
             ***  ** ***: *.*..* *:: :* * *** *** :**. :.* ***:*.********

     human   RIAIARALVRNPKILLLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
     MOUSE   RIAIARALVRNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVIAHRLSTVRNADV 596
50   LPO-3   RIAIARALVKNPKILLLDEATSALDTEAEREVQGALDQAQAGRTTIIVAHRLSTIRNVDR 597
             *********:*****************:*  ** ***:*: *****::******:**.*

     human   IAGFDDGVIVEKGNHDELMKEKGIYFKLVTMQTAGNEVELENAADESKSEIDALEMSSND 657
     MOUSE   IAGFDGGVIVEQGNHDELMREKGIYFKLVMTQTRGNEIEPGNNAYGSQSDTDASELTSEE 656
55   LPO-3   IFVFKAGNIVESGSHEELMSKQGIFYDMTQAQVVRQQQQ--------EAGKDIEDTISES 649
             *  *. * ***.*.*:*** ::**::.:.  *.  :: :  . :  :::  *  :  *:.
```

Fig. 12G

```
     human          SRSSLIRKRSTRRSVRGSQAQDRKLSTKEALDESIPPVSFWRIMKLNLTEWPYFVVGVFC 717
     MOUSE          SKSPLIR-RSIYRSVHRKQDQERRLSMKEAVDEDVPLVSFWRILNLNLSEWPYLLVGVLC 715
  5  LPO-3          AHSHLSRKSSTRSAIS--IATSIHQLAEEVEECKAPPTSMFKIFKFNGDKVGWFIGGIFG 707
                    ::* * *. *   ::  .   . :   :*. : . * .*:::*:::*  :  ::: *::

     human          AIINGGLQPAFAIIFSKIIGVFTRIDDPETKRQNSNLFSLLFLALGIISFITFFLQGFTF 777
     MOUSE          AVINGCIQPVFAIVFSRIVGVFSRDDDHETKRQNCNLFSLFFLVMGLISFVTYFFQGFTF 775
 10  LPO-3          AFIFGSVTPVFALVYAEIFNVYSLPAD--QMQANVYFWCGMFVLMGITFFVGFFTSANCL 765
                    *.* * : *.**:::::.*..*::   * .  : *  ::. :*: :*:  *: :* ..  :

     human          GKAGEILTKRLRYMVFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAVIT 837
     MOUSE          GKAGEILTKRVRYMVFKSMLRQDISWFDDHKNSTGSLTTRLASDASSVKGAMGARLAVVT 835
 15  LPO-3          GRCGESLTMKLRFEAFKNLLRQDIAFYDDLRHGTGKLCTRFATDAPNVR-YVFTRLPVVL 824
                    *:.** ** ::*: .*:.:****::::** :: ** * **:*.**..*:. : :**.*:

     human          QNIANLGTGIIISFIYGWQLTLLLLAIVPIIAIAGVVEMKMLSGQALKDKKELEGAGKIA 897
     MOUSE          QNVANLGTGVILSLVYGWQLTLLLVVIIPLIVLGGIIEMKLLSGQALKDKKQLEISGKIA 895
 20  LPO-3          ASIVTICGALGIGFYYGWQLALILVVMVPLLVMGGYFEMQMRFGKQIRDTQLLEEAGKVA 884
                     .:..:  .: :.: *****:*:*:.::*::.:.* .**::  *: ::*.: ** :**:*

     human          TEAIENFRTVVSLTQEQKFEHMYAQSLQVPYRNSLRKAHIFGITFSFTQAMMYFSYAGCF 957
     MOUSE          TEAIENFRTIVSLTREQKFETMYAQSLQVPYRNAMKKAHVFGITFSFTQAMMYFSYAACF 955
 25  LPO-3          SQAVEHIRTVHSLNRQEQFHFTYCEYLREPFNTNLKHAHTYGAVFAFSQSLIFFMYAAAF 944
                    ::*:*::**: **.::::*.  *.: *: *:.. :::** :* .*:*:*::::* **..*

     human          RFGAYLVAHKLMSFEDVLLVFSAVVFGAMAVGQVSSFAPDYAKAKISAAHIIMIIEKTPL 1017
     MOUSE          RFGAYLVAQQLMTFENVMLVFSAVVFGAMAAGNTSSFAPDYAKAKVSASHIIRIIEKTPE 1015
 30  LPO-3          YLGSIFVNQQAMQPIDVYRVFFAISFCGQMIGNTTSFIPDVVKARLAASLLFYLIEHPTP 1004
                     :*: :* :: *   :*  ** *: * .   *:.:** ** .**:::*: :: :**:..

     human          IDSYSTEGLMPNTLEGNVTFGEVVFNYPTRPDIPVLQGLSLEVKKGQTLALVGSSGCGKS 1077
     MOUSE          IDSYSTEGLKPTLLEGNVKFNGVQFNYPTRPNIPVLQGLSLEVKKGQTLALVGSSGCGKS 1075
 35  LPO-3          IDSLSDSGIVK-PITGNISIRNVFFNYPTRKDTKVLQGFTLDIKAGKTVALVGHSGCGKS 1063
                    *** * .*:  . : **:.:  * ****** :  ****::*::* *:*:**** ******

     human          TVVQLLERFYDPLAGKVLLDGKEIKRLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNS 1137
     MOUSE          TVVQLLERFYDPMAGSVFLDGKEIKQLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNS 1135
 40  LPO-3          TIMGLLERFYNQDKGMIMIDGDNIRNLNISSLREQVCIVSQEPTLFDCTIGENICYGTN- 1122
                    *:: ******:   * :::**.:*:.**:. ** :: ****** ****:*.***.** *:

     human          RVVSQEEIVRAAKEANIHAFIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRQPHIL 1197
     MOUSE          RAVSHEEIVRAAKEANIHQFIDSLPDKYNTRVGDKGTQLSGGQKQRIAIARALVRQPHIL 1195
 45  LPO-3          RNVTYQEIVEAAKMANIHNFILGLPDGYDTHVGEKGTQLSGGQKQRIAIARALVRSPSVL 1182
                    * *: :***.*** **** ** .**: *.*:**:**********************.* :*

     human          LLDEATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGRVKEHGTH 1257
     MOUSE          LLDEATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVIENGKVKEHGTH 1255
 50  LPO-3          LLDEATSALDTESEKIVQEALDAAKQGRTCLVIAHRLSTIQNSDVIAIVSEGKIVEKGTH 1242
                    ***************:****** *::****:***********:*:*.:..:*:: *:***

     human          QQLLAQKGIYFSMVSVQAGTKRQ 1280
     MOUSE          QQLLAQKGIYFSMV--QAGAKRS 1276
 55  LPO-3          DELIRKSEIYQKFCETQRIVESQ 1265
                    ::*: :.
```

Fig. 12G Cont.

Fig. 13A

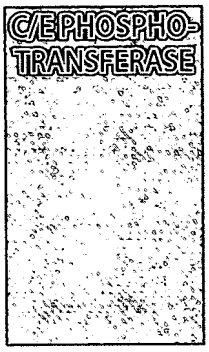

Fig. 13B

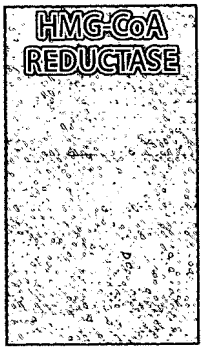

Fig. 13C

Fig. 13D

Fig. 13E

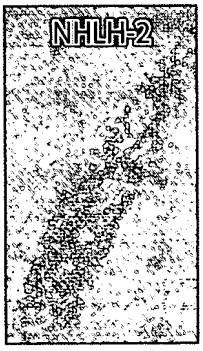

Fig. 13F